

U.S NAT

1ST STAGE WORKSHEET

(EQ)

U.S. APPL. NO. 10/567749

INTERNATIONAL APPL. EP04/008470

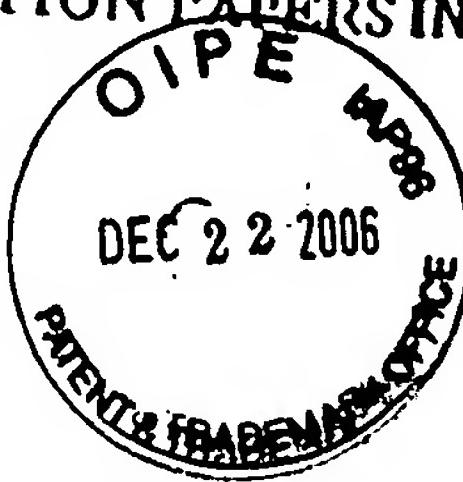
APPLICATION FILED BY: 20 MOS.

OR 30 MOS.

SCREENED BY

INTERNATIONAL APPLICATION PAPERS IN THE APPLICATION FILE:

- International application
- Article 19 amendments
- Priority Document(s) No. 3
- Request Form PCT/RO/101
- PCT/IB/302
- PCT/IB/304
- PCT/IB/306
- PCT/IB/308
- PCT/IB/331
- OTHER PCT/IB 237
- PCT/TPBA/409 also 416



- 409 annexes to IPER
- PCT/ISA/210 (Search report)
- Search report References
- Other Papers filed

WIPO PUBLICATION
PUBLICATION NO. WO 05/014843
PUBLICATION DATE 17.02.05
PUBLICATION LANG. ENGLISH
NOT PUBLISHED
U.S. only Requested

RECEIVED FROM THE APPLICANT: (other than checked above)

International application basic fee paid

Express Processing Requested

Translation of the International Application

Send the IB copy of the IA

Description

Claims

Drawings

Foreign Language in drawing

Article 19 Amendments

Amendment used in application

Article 34 Amendment

Amendment used in application

IA

IA transaction done

- Preliminary Amendment(s) filed 10 FEB 2005
- second submission
- Information Disclosure Statement
- second submission
- Assignment
- Forward to Assignment Branch
- Substitute Specification 10 FEB 2005
- Small Entity Statement
- type
- Oath/Declaration (date submitted) 10 FEB 2005
- Not executed
- Executed
- Power of Attorney
- Change of Address

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C Receipt of Request (PTO-1399 Transmittal Letter)	<u>10 FEB 2005</u>
Acceptable oath/declaration received	<u>10 FEB 2005</u>
Date	<u>10 FEB 2005</u>
Complete 35 USC 371 requirements met	<u>10 FEB 2005</u>
DATE NOTICE COMPLETED	<u>10 FEB 2005</u>
903 Notice of Acceptance	
905 Notice of Missing Requirements	
917 Notice of A defective oath or declaration	
916 Notice of defective response	

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STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/567,749
Source: IFWP
Date Processed by STIC: 02/28/2006

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
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FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

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Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>), EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
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Revised 01/10/06

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IFWP



RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/567,749

DATE: 02/28/2006

TIME: 12:03:09

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Output Set: N:\CRF4\02282006\J567749.raw

3 <110> APPLICANT: Degussa AG <120> Process for the preparation of L-threonine <130>

030235

C--> 4 <140> CURRENT APPLICATION NUMBER: US/10/567,749

C--> 4 <141> CURRENT FILING DATE: 2006-02-10

E--> 4 <160> NUMBER OF SEQ ID: 10 <170> PatentIn version 3.1<210> 1<211> 993<212> DNA<213>

ERRORED SEQUENCES

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E--> 93

E--> 93

E--> 93

E--> 93 <400> SEQUENCE:

Does Not Comply
Corrected Diskette Needed

(Prg-1-11)

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94	1					5			10				15			
95	Phe	Asp	Glu	Asn	Gly	Val	Glu	Val	Phe	Asp	Glu	Lys	Ala	Leu	Val	Glu
96						20			25				30			
97	Gln	Glu	Pro	Ser	Asp	Asn	Asp	Leu	Ala	Glu	Glu	Glu	Leu	Leu	Ser	Gln
98						35			40				45			
99	102	Gly	Ala	Thr	Gln	Arg	Val	Leu	Asp	Ala	Thr	Gln	Leu	Tyr	Leu	Glu
100	103						50		55			60				
101	105	Ile	Gly	Tyr	Ser	Pro	Leu	Leu	Thr	Ala	Glu	Glu	Val	Tyr	Phe	Ala
102	106						65		70		75		80			
103	107	Arg	Arg	Ala	Leu	Arg	Gly	Asp	Val	Ala	Ser	Arg	Arg	Arg	Met	Ile
104	108						85		90		95					
105	109	Ser	Asn	Leu	Arg	Leu	Val	Val	Lys	Ile	Ala	Arg	Arg	Tyr	Gly	Asn
106	110						100		105		110					
107	111	Gly	Leu	Ala	Leu	Leu	Asp	Leu	Ile	Glu	Glu	Gly	Asn	Leu	Gly	Ile
108	112						115		120		125					
109	113	Arg	Ala	Val	Glu	Lys	Phe	Asp	Pro	Glu	Arg	Gly	Phe	Arg	Phe	Ser
110	114						130		135		140					
111	115	Tyr	Ala	Thr	Trp	Trp	Ile	Arg	Gln	Thr	Ile	Glu	Arg	Ala	Ile	Met
112	116						145		150		155		160			
113	117	Gln	Thr	Arg	Thr	Ile	Arg	Leu	Pro	Ile	His	Ile	Val	Lys	Glu	Leu
114	118						165		170		175					
115	119	127	Val	Tyr	Leu	Arg	Thr	Ala	Arg	Glu	Leu	Ser	His	Lys	Leu	Asp
116	120						180		185		190					
117	121	130	Pro	Ser	Ala	Glu	Glu	Ile	Ala	Glu	Gln	Leu	Asp	Lys	Pro	Val
118	122						195		200		205					
119	123	131	133	Val	Ser	Arg	Met	Leu	Arg	Leu	Asn	Glu	Arg	Ile	Thr	Ser
120	124						210		215		220					

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136 Pro Leu Gly Gly Asp Ser Glu Lys Ala Leu Leu Asp Ile Leu Ala Asp
 137 225 230 235 240
 139 Glu Lys Glu Asn Gly Pro Glu Asp Thr Thr Gln Asp Asp Asp Met Lys
 140 245 250 255
 142 Gln Ser Ile Val Lys Trp Leu Phe Glu Leu Asn Ala Lys Gln Arg Glu
 143 260 265 270
 145 Val Leu Ala Arg Arg Phe Gly Leu Leu Gly Tyr Glu Ala Ala Thr Leu
 146 275 280 285
 148 Glu Asp Val Gly Arg Glu Ile Gly Leu Thr Arg Glu Arg Val Arg Gln
 149 290 295 300
 151 Ile Gln Val Glu Gly Leu Arg Arg Leu Arg Glu Ile Leu Gln Thr Gln
 152 305 310 315 320
 154 Gly Leu Asn Ile Glu Ala Leu Phe Arg Glu
 155 325 *hard return Enter*

E--> 157 <210> SEQ ID NO: 3<211> 993<212> DNA<213> Escherichia coli<220><221> Allele<222>
 158 <223> OTHER INFORMATION: rpos allele

W--> 160 <

E--> 162 .

V--> 162 .

S--> 162 .

162 <400> SEQUENCE: 3

163 atgagtcaga atacgctgaa agttcatgat tttaaatgaag atgcggatt tgatgagaac 60
 165 ggagtgtgagg ttttgacga aaaggccta gtagaatagg aacccagtga taacgatttg 120
 167 gccgaagagg aactgttatac gcagggagcc acacagcgtg tggggacgc gactcagctt 180
 169 taccttggtg agattggta ttcaccactg ttaacggccg aagaagaagt ttatggcg 240
 171 cgtcgccac tgcgtggaga tgcgtggata cgccgcggta tgatcgagag taacttgcgt 300
 173 ctgggtgtaa aaattgccccg ccgttatggc aatcggtgtc tggcggttgc ggaccttatac 360
 175 gaagagggca acctggggct gatccgcgcg gtagagaagt ttgaccggaa acgtggtttc 420
 177 cgcttctcaa catacgcaac ctgggtggatt cgccagacga ttgaacgggc gattatgaac 480
 179 caaacccgtt ctattcgaaa gcccattcac atcgtaaagg agctgaacgt ttacctgcga 540
 181 accgcacgtg agttgtccca taagctggac catgaaccaa gtgcggaaaga gatcgacag 600
 183 caactggata agccagttga tgacgtcagc cgtatgttc gtcttaacga ggcattacc 660
 185 tcggtagaca ccccgctggg tgggtattcc gaaaaagcgt tgctggacat cctggccgat 720
 187 gaaaaagaga acggccggaa agataccacg caagatgacg atatgaagca gagcatgtc 780
 189 aaatggctgt tcgagctgaa cgccaaacag cgtgaagtgc tggcacgtcg attcggtttg 840
 191 ctgggtacg aagcgcaac actggaaagat gtaggtcgta aaattggcct caccgtgaa 900
 193 cgtgtcgcc agattcaggt tgaaggcctg cgccgttgc gcgaaatcct gcaaacgcag 960
 195 gggctgaata tcgaagcgct gttcccgag taa 993

E--> 197 <210> SEQ ID NO: 4<211> 75<212> DNA<213> Escherichia coli<220><221> tRNA<222>
 198 <223> OTHER INFORMATION: supE allele

E--> 200 <

E--> 200 .

E--> 200 .

200 <400> SEQUENCE: 4

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 203 ctcgtacccc agccca 75

E--> 207 <210> SEQ ID NO: 5<211> 1545<212> DNA<213> Escherichia coli<220><221> CDS<222>
 208 <223> OTHER INFORMATION: ilvA-Gen

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PATENT APPLICATION: US/10/567,749

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TIME: 12:03:09

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 211 atg gct gac tcg caa ccc ctg tcc ggt gct ccg gaa ggt gcc gaa tat 48
 212 Met Ala Asp Ser Gln Pro Leu Ser Gly Ala Pro Glu Gly Ala Glu Tyr
 213 1 5 10 15
 215 tta aga gca gtg ctg cgc gcg ccg gtt tac gag gca gcg cag gtt acg 96
 216 Leu Arg Ala Val Leu Arg Ala Pro Val Tyr Glu Ala Ala Gln Val Thr
 217 20 25 30
 219 ccg cta caa aaa atg gaa aaa ctg tcg tcg cgt ctt gat aac gtc att 144
 220 Pro Leu Gln Lys Met Glu Lys Leu Ser Ser Arg Leu Asp Asn Val Ile
 221 35 40 45
 223 ctg gtg aag cgc gaa gat cgc cag cca gtg cac acg ttt aag ctg cgc 192
 224 Leu Val Lys Arg Glu Asp Arg Gln Pro Val His Ser Phe Lys Leu Arg
 225 50 55 60
 227 ggc gca tac gcc atg atg gcg ggc ctg acg gaa gaa cag aaa gcg cac 240
 228 Gly Ala Tyr Ala Met Met Ala Gly Leu Thr Glu Glu Gln Lys Ala His
 229 65 70 75 80
 231 gac atc act ctc tct gcg ggt aac gac gcg cag ggc ttc gcg ttt 299
 232 Gly Val Ile Thr Ala Ser Ala Gly Asn His Ala Gln Gly Val Ala Phe
 233 85 90 95
 235 tct tct gcg cgg tta ggc gtg aag gcc ctg atc gtt atg cca acc gcc 336
 236 Ser Ser Ala Arg Leu Gly Val Lys Ala Leu Ile Val Met Pro Thr Ala
 237 100 105 110
 239 acc gcc gac atc aaa gtc gac gcg gtg cgc ggc ttc ggc ggc gaa gtg 384
 240 Thr Ala Asp Ile Lys Val Asp Ala Val Arg Gly Phe Gly Gly Glu Val
 241 115 120 125
 243 ctg ctc cac ggc gcg aac ttt gat gaa gcg aaa gcc aaa gcg atc gaa 432
 244 Leu Leu His Gly Ala Asn Phe Asp Glu Ala Lys Ala Lys Ala Ile Glu
 245 130 135 140
 247 ctg tca cag cag ggg ttc acc tgg gtg ccg ccg ttc gac cat ccg 480
 248 Leu Ser Gln Gln Gly Phe Thr Trp Val Pro Pro Phe Asp His Pro
 249 145 150 155 160
 251 atg gtg att gcc ggg caa ggc acg ctg gcg ctg gaa ctg ctc cag cag 528
 252 Met Val Ile Ala Gly Gln Gly Thr Leu Ala Leu Glu Leu Leu Gln Gln
 253 165 170 175
 255 gac gcc cat ctc gac cgc gta ttt gtg cca gtc ggc ggc ggc ggt ctg 576
 256 Asp Ala His Leu Asp Arg Val Phe Val Pro Val Gly Gly Gly Leu
 257 180 185 190
 259 gct gct ggc gtg gcg gtg ctg atc aaa caa ctg atg ccg caa atc aaa 624
 260 Ala Ala Gly Val Ala Val Leu Ile Lys Gln Leu Met Pro Gln Ile Lys
 261 195 200 205
 264 gtg atc gcc gta gaa gcg gaa gac tcc gcc tgc ctg aaa gca gcg ctg 672
 265 Val Ile Ala Val Glu Ala Glu Asp Ser Ala Cys Leu Lys Ala Ala Leu
 266 210 215 220
 268 gat gcg ggt cat ccg gtt gat ctg ccg cgc gta ggg cta ttt gct gaa 720
 269 Asp Ala Gly His Pro Val Asp Leu Pro Arg Val Gly Leu Phe Ala Glu
 270 225 230 235 240
 272 ggc gta gcg gta aaa cgc atc ggt gac gaa acc ttc cgt tta tgc cag 768

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273	Gly Val Ala Val Lys Arg Ile Gly Asp Glu Thr Phe Arg Leu Cys Gln			
274	245	250	255	
276	gag tat ctc gac gac atc atc acc gtc gat agc gat gcg atc tgt gcg	816		
277	Glu Tyr Leu Asp Asp Ile Ile Thr Val Asp Ser Asp Ala Ile Cys Ala			
278	260	265	270	
280	gcg atg aag gat tta ttc gaa gat gtg cgc gcg gtg gaa ccc tct	864		
281	Ala Met Lys Asp Leu Phe Glu Asp Val Arg Ala Val Ala Glu Pro Ser			
282	275	280	285	
284	ggc gcg ctg gcg ctg gcg gga atg aaa aaa tat atc gcc ctg cac aac	912		
285	Gly Ala Leu Ala Leu Ala Gly Met Lys Lys Tyr Ile Ala Leu His Asn			
286	290	295	300	
288	att cgc ggc gaa cgg ctg gcg cat att ctt tcc ggt gcc aac gtg aac	960		
289	Ile Arg Gly Glu Arg Leu Ala His Ile Leu Ser Gly Ala Asn Val Asn			
290	305	310	315	320
292	tcc cac ggc ctg cgc tac gtc tca gaa cgc tgc gaa ctg ggc gaa cag	1008		
293	Phe His Gly Leu Arg Tyr Val Ser Glu Arg Cys Glu Leu Gly Glu Gln			
294	325	330	335	
296	cgt gaa gcg ttg ttg gcg gtg acc att ccg gaa gaa aaa ggc agc ttc	1056		
297	Arg Cys Ala Leu Leu Ala Val Thr Ile Pro Glu Gln Lys Gly Ser Phe			
298	340	345	350	
300	ctc aaa ttc tgc caa ctg ctt ggc ggg cgt tcg gtc acc gag ttc aac	1104		
301	Leu Lys Phe Cys Gln Leu Leu Gly Gly Arg Ser Val Thr Glu Phe Asn			
302	355	360	365	
304	tac cgt ttt gcc gat gcc aaa aac gcc tgc atc ttt gtc ggt gtg cgc	1152		
305	Tyr Arg Phe Ala Asp Ala Lys Asn Ala Cys Ile Phe Val Gly Val Arg			
306	370	375	380	
308	ctg agc cgc ggc ctc gaa gag cgc aaa gaa att ttg cag atg ctc aac	1200		
309	Leu Ser Arg Gly Leu Glu Glu Arg Lys Glu Ile Leu Gln Met Leu Asn			
310	385	390	395	400
312	gac ggc ggc tac agc gtg gtt gat ctc tcc gac gac gaa atg gcg aag	1248		
313	Asp Gly Gly Tyr Ser Val Val Asp Leu Ser Asp Asp Glu Met Ala Lys			
314	405	410	415	
316	cta cac gtg cgc tat atg gtc ggc gga cgt cca tcg cat ccg ttg cag	1296		
317	Leu His Val Arg Tyr Met Val Gly Gly Arg Pro Ser His Pro Leu Gln			
318	420	425	430	
320	gaa cgc ctc tac agc ttc gaa ttc ccg gaa tca ccg ggc gcg ctg ctg	1344		
321	Glu Arg Leu Tyr Ser Phe Glu Phe Pro Glu Ser Pro Gly Ala Leu Leu			
322	435	440	445	
324	cgc ttc ctc aac acg ctg ggt acg tac tgg aac att tct ttg ttc cac	1392		
325	Arg Phe Leu Asn Thr Leu Gly Thr Tyr Trp Asn Ile Ser Leu Phe His			
326	450	455	460	
329	tat cgc agc cat ggc acc gac tac ggg cgc gta ctg gcg gcg ttc gaa	1440		
330	Tyr Arg Ser His Gly Thr Asp Tyr Gly Arg Val Leu Ala Ala Phe Glu			
331	465	470	475	480
333	ctt ggc gac cat gaa ccg gat ttc gaa acc ccg ctg aat gag ctg ggc	1488		
334	Leu Gly Asp His Glu Pro Asp Phe Glu Thr Arg Leu Asn Glu Leu Gly			
335	485	490	495	
337	tac gat tgc cac gac gaa acc aat aac ccg gcg ttc agg ttc ttt ttg	1536		
338	Tyr Asp Cys His Asp Glu Thr Asn Asn Pro Ala Phe Arg Phe Leu			

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339 500 505 510 1545

341 gcg ggt tag
342 Ala Gly
E--> 345 <210> SEQ ID NO: 6<211> 514<212> PRT<213> Escherichia coli

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E--> 346 --

E--> 346 .

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 351 20 25 30
 353 Pro Leu Gln Lys Met Glu Lys Leu Ser Ser Arg Leu Asp Asn Val Ile
 354 35 40 45
 356 Leu Val Lys Arg Glu Asp Arg Gln Pro Val His Ser Phe Lys Leu Arg
 357 50 55 60
 359 Gly Ala Tyr Ala Met Met Ala Gly Leu Thr Glu Glu Gln Lys Ala His
 360 65 70 75 80
 362 Gly Val Ile Thr Ala Ser Ala Gly Asn His Ala Glu Gly Val Ala Phe
 363 85 90 95
 365 Ser Ser Ala Arg Leu Gly Val Lys Ala Leu Ile Val Met Pro Thr Ala
 366 100 105 110
 368 Thr Ala Asp Ile Lys Val Asp Ala Val Arg Gly Phe Gly Gly Glu Val
 369 115 120 125
 371 Leu Leu His Gly Ala Asn Phe Asp Glu Ala Lys Ala Lys Ala Ile Glu
 372 130 135 140
 374 Leu Ser Gln Gln Gly Phe Thr Trp Val Pro Pro Phe Asp His Pro
 375 145 150 155 160
 377 Met Val Ile Ala Gly Gln Gly Thr Leu Ala Leu Glu Leu Leu Gln Gln
 378 165 170 175
 380 Asp Ala His Leu Asp Arg Val Phe Val Pro Val Gly Gly Gly Leu
 381 180 185 190
 383 Ala Ala Gly Val Ala Val Leu Ile Lys Gln Leu Met Pro Gln Ile Lys
 384 195 200 205
 386 Val Ile Ala Val Glu Ala Glu Asp Ser Ala Cys Leu Lys Ala Ala Leu
 387 210 215 220
 390 Asp Ala Gly His Pro Val Asp Leu Pro Arg Val Gly Leu Phe Ala Glu
 391 225 230 235 240
 393 Gly Val Ala Val Lys Arg Ile Gly Asp Glu Thr Phe Arg Leu Cys Gln
 394 245 250 255
 396 Glu Tyr Leu Asp Asp Ile Ile Thr Val Asp Ser Asp Ala Ile Cys Ala
 397 260 265 270
 399 Ala Met Lys Asp Leu Phe Glu Asp Val Arg Ala Val Ala Glu Pro Ser
 400 275 280 285
 402 Gly Ala Leu Ala Leu Ala Gly Met Lys Lys Tyr Ile Ala Leu His Asn
 403 290 295 300
 405 Ile Arg Gly Glu Arg Leu Ala His Ile Leu Ser Gly Ala Asn Val Asn
 406 305 310 315 320
 408 Phe His Gly Leu Arg Tyr Val Ser Glu Arg Cys Glu Leu Gly Glu Gln

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Input Set : A:\pto.da.txt
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409	325	330	335
411 Arg	Glu Ala Leu	Leu Ala Val Thr Ile Pro	Glu Glu Lys Gly Ser Phe
412	340	345	350
414 Leu Lys	Phe Cys Gln	Leu Leu Gly Gly Arg Ser Val	Thr Glu Phe Asn
415	355	360	365
417 Tyr Arg	Phe Ala Asp Ala	Lys Asn Ala Cys Ile Phe Val	Gly Val Arg
418	370	375	380
420 Leu Ser	Arg Gly Leu	Glu Glu Arg Lys Glu Ile	Leu Gln Met Leu Asn
421	385	390	395
423 Asp Gly	Gly Tyr Ser Val Val	Asp Leu Ser Asp Asp	Glu Met Ala Lys
424	405	410	415
426 Leu His	Val Arg Tyr Met Val	Gly Gly Arg Pro Ser His	Pro Leu Gln
427	420	425	430
429 Glu Arg	Leu Tyr Ser Phe	Glu Phe Pro Glu Ser Pro	Gly Ala Leu Leu
430	435	440	445
432 Arg Phe	Leu Asn Thr Leu	Gly Thr Tyr Trp Asn	Ile Ser Leu Phe His
433	450	455	460
435 Tyr Arg	Ser His Gly Thr Asp	Tyr Gly Arg Val	Leu Ala Ala Phe Glu
436	465	470	475
438 Leu	Gly Asp His Glu	Asp His Glu Thr Arg	Leu Asn Glu Leu Gly
439	485	490	495
441 Tyr Asp	Cys His Asp Glu Thr Asn Asn	Pro Ala Phe Arg	Phe Phe Leu
442	500	505	510
444 Ala	Gly		

E--> 447 <210> SEQ ID NO: 7<211> 1545<212> DNA<213> Escherichia coli

W--> 449

W--> 452

E--> 455

E--> 455

E--> 455 <213> ORGANISM:

455 <400> SEQUENCE: 7

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457 Met	Ala Asp	Ser Gln	Pro Leu	Ser Gly	Ala Pro Glu Gly Ala Glu Tyr
458 1	5	10	15		
460 tta	aga gca	gtg ctg	cgc gcg	ccg gtt tac	gag gcg gcg cag gtt acg
461 Leu	Arg Ala	Val Leu	Arg Ala	Pro Val	Tyr Glu Ala Ala Gln Val Thr
462	20	25	30		
464 ccg	cta caa	aaa atg	gaa aaa	ctg tcg	cgt ctt gat aac gtc att
465 Pro	Leu Gln	Lys Met	Glu Lys	Leu Ser	Ser Arg Leu Asp Asn Val Ile
466	35	40	45		
468 ctg	gtg aag	cgc gaa	aat cgc	cag cca	gtg cac agc ttt aag ctg cgc
469 Leu Val	Lys Arg	Glu Asp	Arg Gln	Pro Val	His Ser Phe Lys Leu Arg
470	50	55	60		
472 ggc	gca tac	gcc atg	atg gcg	ggc ctg	acg gaa gaa cag aaa gcg cac
473 Gly	Ala Tyr	Ala Met	Met Ala	Gly Leu	Thr Glu Gln Lys Ala His
474 65	70	75	80		
476 ggc	gtg atc	act gct	tct gcg	ggt aac cac	gac gcg cag ggc gtc gcg ttt
477 Gly Val	Ile Thr	Ala Ser	Ala Gly	Asn His Ala Gln	Gly Val Ala Phe
478	85	90	95		

same error
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481	Ser	Ser	Ala	Arg	Leu	Gly	Val	Lys	Ala	Leu	Ile	Val	Met	Pro	Thr	Ala	
482				100					105				110				
484	acc	gcc	gac	atc	aaa	gtc	gac	gcf	gtg	cgc	ggc	ttc	ggc	ggc	gaa	gtg	384
485	Thr	Ala	Asp	Ile	Lys	Val	Asp	Ala	Val	Arg	Gly	Phe	Gly	Gly	Glu	Val	
486				115					120			125					
488	ctg	ctc	cac	ggc	gcf	aac	ttt	gat	gaa	gcf	aaa	gcc	aaa	gcf	atc	gaa	432
489	Leu	Leu	His	Gly	Ala	Asn	Phe	Asp	Glu	Ala	Lys	Ala	Lys	Ala	Ile	Glu	
490				130				135			140						
492	ctg	tca	cag	cag	cag	ggg	ttc	acc	tgg	gtg	ccg	ccg	ttc	gac	cat	ccg	480
493	Leu	Ser	Gln	Gln	Gly	Phe	Thr	Trp	Val	Pro	Pro	Phe	Asp	His	Pro		
494				145				150		155		160					
496	atg	gtg	att	gcc	ggg	caa	ggc	acg	ctg	gcf	ctg	gaa	ctg	ctc	cag	cag	528
497	Met	Val	Ile	Ala	Gly	Gln	Gly	Thr	Leu	Ala	Leu	Glu	Leu	Leu	Gln	Gln	
498				165				170			175						
500	gac	gcc	cat	ctc	gac	cgc	gta	ttt	gtg	cca	gtc	ggc	ggc	ggc	ggt	ctg	576
501	Asp	Ala	His	Leu	Asp	Arg	Val	Phe	Val	Pro	Val	Gly	Gly	Gly	Gly	Leu	
502				180				185			190						
504	gct	gtc	ggc	gtc	ggc	gtc	atc	aaa	caa	atg	ccg	caa	atc	aaa		624	
505	Ala	Gly	Val	Ala	Val	Leu	Ile	Lys	Gln	Leu	Met	Pro	Gln	Ile	Lys		
506				195				200			205						
509	gtg	atc	gcc	gta	gaa	gcf	gaa	gac	tcc	gcc	tgc	ctg	aaa	gca	gcf	ctg	672
510	Val	Ile	Ala	Val	Glu	Ala	Glu	Asp	Ser	Ala	Cys	Leu	Lys	Ala	Ala	Leu	
511				210				215			220						
513	gat	gcf	ggt	cat	ccg	gtt	gat	ctg	ccg	gcf	gta	ggg	cta	ttt	gct	gaa	720
514	Asp	Ala	Gly	His	Pro	Val	Asp	Leu	Pro	Arg	Val	Gly	Leu	Phe	Ala	Glu	
515				225				230		235		240					
517	ggc	gta	gcf	gta	aaa	cgc	atc	ggt	gac	gaa	acc	tcc	cgt	tta	tgc	cag	768
518	Gly	Val	Ala	Val	Lys	Arg	Ile	Gly	Asp	Glu	Thr	Phe	Arg	Leu	Cys	Gln	
519				245				250			255						
521	gag	tat	ctc	gac	gac	atc	atc	acc	gtc	gat	agc	gat	gcf	atc	tgt	gcf	816
522	Glu	Tyr	Leu	Asp	Asp	Ile	Ile	Thr	Val	Asp	Ser	Asp	Ala	Ile	Cys	Ala	
523				260				265			270						
525	gcf	atg	aag	gat	tta	tcc	gaa	gat	gtg	ccg	gcf	gtg	gcf	aaa	ccc	tct	864
526	Ala	Met	Lys	Asp	Leu	Phe	Glu	Asp	Val	Arg	Ala	Val	Ala	Lys	Pro	Ser	
527				275				280		285							
529	ggc	gcf	ctg	gcf	ctg	gcf	gga	atg	aaa	aaa	tat	atc	gcc	ctg	cac	aac	912
530	Gly	Ala	Leu	Ala	Leu	Ala	Gly	Met	Lys	Lys	Tyr	Ile	Ala	Leu	His	Asn	
531				290				295			300						
533	att	ccg	ggc	gaa	cgf	ctg	gcf	cat	att	tcc	ggt	gcc	aac	gtg	aac		960
534	Ile	Arg	Gly	Glu	Arg	Leu	Ala	His	Ile	Leu	Ser	Gly	Ala	Asn	Val	Asn	
535				305				310		315		320					
537	tcc	cac	ggc	ctg	ccg	tac	gtc	tca	gaa	ccg	tgc	gaa	ctg	ggc	gaa	cag	1008
538	Phe	His	Gly	Leu	Arg	Tyr	Val	Ser	Glu	Arg	Cys	Glu	Leu	Gly	Glu	Gln	
539				325				330			335						
541	cgt	gaa	gcf	ttg	ttg	gcf	gtg	acc	att	ccg	gaa	gaa	aaa	ggc	agc	ttc	1056
542	Arg	Glu	Ala	Leu	Leu	Ala	Val	Thr	Ile	Pro	Glu	Glu	Lys	Gly	Ser	Phe	
543				340				345			350						
545	ctc	aaa	ttc	tgc	caa	ctg	ctt	ggc	ggg	cgt	tgc	gtc	acc	gag	ttc	aac	1104

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Input Set : A:\pto.da.txt
Output Set: N:\CRP4\02282006\J567749.raw

546 Leu Lys Phe Cys Gln Leu Leu Gly Gly Arg Ser Val Thr Glu Phe Asn
 547 355 360 365
 549 tac cgt ttt gcc gat gcc aaa aac gcc tgc atc ttt gtc ggt gtg cgc 1152
 550 Tyr Arg Phe Ala Asp Ala Lys Asn Ala Cys Ile Phe Val Gly Val Arg
 551 370 375 380
 553 ctg agc cgc ggc ctc gaa gag cgc aaa gaa att ttg cag atg ctc aac 1200
 554 Leu Ser Arg Gly Leu Glu Glu Arg Lys Glu Ile Leu Gln Met Leu Asn
 555 385 390 395 400
 557 gac ggc ggc tac agc gtg gtt gat ctc tcc gac gac gaa atg gcg aag 1248
 558 Asp Gly Gly Tyr Ser Val Val Asp Leu Ser Asp Asp Glu Met Ala Lys
 559 405 410 415
 561 cta cac gtg cgc tat atg gtc ggc gga cgt cca tcg cat ccg ttg cag 1296
 562 Leu His Val Arg Tyr Met Val Gly Gly Arg Pro Ser His Pro Leu Gln
 563 420 425 430
 565 gaa cgc ctc tac agc ttc gaa ttc ccg gaa tca ccg ggc gcg ctg ctg 1344
 566 Glu Arg Leu Tyr Ser Phe Glu Phe Pro Glu Ser Pro Gly Ala Leu Leu
 567 435 440 445
 569 cgc ttc ctc aac acg ctg ggt acg tac tgg aac att tct ttg ttc cac 1392
 570 Arg Phe Val Asn Thr Leu Gly Thr Tyr Tyr Asn Ile Ser Leu Phe His
 571 450 455 460
 574 tat cgc agc cat ggc acc gac tac ggg cgc gta ctg gcg gcg ttc gaa 1440
 575 Tyr Arg Ser His Gly Thr Asp Tyr Gly Arg Val Leu Ala Ala Phe Glu
 576 465 470 475 480
 578 ctt ggc gac cat gaa ccg gat ttc gaa acc ccg ctg aat gag ctg ggc 1488
 579 Leu Gly Asp His Glu Pro Asp Phe Glu Thr Arg Leu Asn Glu Leu Gly
 580 485 490 495
 582 tac gat tgc cac gac gaa acc aat aac ccg gcg ttc agg ttc ttt ttg 1536
 583 Tyr Asp Cys His Asp Glu Thr Asn Asn Pro Ala Phe Arg Phe Phe Leu
 584 500 505 510
 586 gcg ggt tag
 587 Ala Gly *hand Return Berlin*
 590 <210> SEQ ID NO: 8<211> 514<212> PRT<213> Escherichia coli
 591
 591
 591
 591 <400> SEQUENCE: 8
 592 Met Ala Asp Ser Gln Pro Leu Ser Gly Ala Pro Glu Gly Ala Glu Tyr
 593 1 5 10 15
 595 Leu Arg Ala Val Leu Arg Ala Pro Val Tyr Glu Ala Ala Gln Val Thr
 596 20 25 30
 598 Pro Leu Gln Lys Met Glu Lys Leu Ser Ser Arg Leu Asp Asn Val Ile
 599 35 40 45
 601 Leu Val Lys Arg Glu Asp Arg Gln Pro Val His Ser Phe Lys Leu Arg
 602 50 55 60
 604 Gly Ala Tyr Ala Met Met Ala Gly Leu Thr Glu Glu Gln Lys Ala His
 605 65 70 75 80
 607 Gly Val Ile Thr Ala Ser Ala Gly Asn His Ala Gln Gly Val Ala Phe
 608 85 90 95
 610 Ser Ser Ala Arg Leu Gly Val Lys Ala Leu Ile Val Met Pro Thr Ala

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Input Set : A:\pto.da.txt
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611	100	105	110
613	Thr Ala Asp Ile Lys Val Asp Ala Val Arg Gly Phe Gly Gly Glu Val		
614	115	120	125
616	Leu Leu His Gly Ala Asn Phe Asp Glu Ala Lys Ala Lys Ala Ile Glu		
617	130	135	140
619	Leu Ser Gln Gln Gln Gly Phe Thr Trp Val Pro Pro Phe Asp His Pro		
620	145	150	155
622	Met Val Ile Ala Gly Gln Gly Thr Leu Ala Leu Glu Leu Leu Gln Gln		160
623	165	170	175
625	Asp Ala His Leu Asp Arg Val Phe Val Pro Val Gly Gly Gly Leu		
626	180	185	190
629	Ala Ala Gly Val Ala Val Leu Ile Lys Gln Leu Met Pro Gln Ile Lys		
630	195	200	205
632	Val Ile Ala Val Glu Ala Asp Ser Ala Cys Leu Lys Ala Ala Leu		
633	210	215	220
635	Asp Ala Gly His Pro Val Asp Leu Pro Arg Val Gly Leu Phe Ala Glu		
636	225	230	235
638	Gly Val Ala Val Lys Arg Ile Gly Asp Glu Thr Phe Arg Leu Cys Gln		240
640	245	250	255
541	Glu Tyr Leu Asp Asp Ile Ile Thr Val Asp Ser Asp Ala Ile Cys Ala		
642	260	265	270
644	Ala Met Lys Asp Leu Phe Glu Asp Val Arg Ala Val Ala Lys Pro Ser		
645	275	280	285
647	Gly Ala Leu Ala Leu Ala Gly Met Lys Lys Tyr Ile Ala Leu His Asn		
648	290	295	300
650	Ile Arg Gly Glu Arg Leu Ala His Ile Leu Ser Gly Ala Asn Val Asn		
651	305	310	315
653	Phe His Gly Leu Arg Tyr Val Ser Glu Arg Cys Glu Leu Gly Glu Gln		320
654	325	330	335
656	Arg Glu Ala Leu Leu Ala Val Thr Ile Pro Glu Glu Lys Gly Ser Phe		
657	340	345	350
659	Leu Lys Phe Cys Gln Leu Leu Gly Gly Arg Ser Val Thr Glu Phe Asn		
660	355	360	365
662	Tyr Arg Phe Ala Asp Ala Lys Asn Ala Cys Ile Phe Val Gly Val Arg		
663	370	375	380
665	Leu Ser Arg Gly Leu Glu Glu Arg Lys Glu Ile Leu Gln Met Leu Asn		
666	385	390	395
668	400	405	410
669	Asp Gly Gly Tyr Ser Val Val Asp Leu Ser Asp Asp Glu Met Ala Lys		415
671	415	420	425
672	Leu His Val Arg Tyr Met Val Gly Gly Arg Pro Ser His Pro Leu Gln		430
674	430	435	440
675	Glu Arg Leu Tyr Ser Phe Glu Phe Pro Glu Ser Pro Gly Ala Leu Leu		445
677	445	Arg Phe Leu Asn Thr Leu Gly Thr Tyr Trp Asn Ile Ser Leu Phe His	
678	450	455	460
680	Tyr Arg Ser His Gly Thr Asp Tyr Gly Arg Val Leu Ala Ala Phe Glu		
681	465	470	475
683	Leu Gly Asp His Glu Pro Asp Phe Glu Thr Arg Leu Asn Glu Leu Gly		480
684	475	485	490
			495

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686 Tyr Asp Cys His Asp Glu Thr Asn Asn Pro Ala Phe Arg Phe Phe Leu
687 500 505 510

689 Ala Gly

B--> 692 <210> SEQ ID NO: 9<211> 1548<212> DNA<213> Escherichia coli

W--> 694 <220> FRATURE:<221> DNA<222> (1)..(1548)<223>

W--> 695

E--> 696

E--> 698

E--> 698

698 <400> SEQUENCE: 9

699 tcgcgatctg gtactgtaag gggaaataga gatgacacac gataataaat tgcagggtga	60
701 agctattaaa cgcggcacgg taattgacca tatcccccc cagatcggtt ttaagctgtt	120
703 gagtcgttc aagctgaccg aaacggatca gcgcacacc attggctcga acctgccttc	180
705 tggcgagatg ggccgcaaag atctgatcaa aatcgaaaat accttttga gtgaagatca	240
707 agtagatcaa ctggcattgt atgcgcgcga agccacgggt aaccgtatcg acaactatga	300
709 agtggtggtt aaatcgccc caagtctgcc ggagcgcattc gacaatgtgc tggctgccc	360
711 gaacagcaac tgtatcagcc atgcccacc ggtttcatcc agctttgccg tgcaaaaacg	420
713 cgccaatgtatcgcgtca aatgcaaata ctgtgaaaaa gagtttccc ataatgttgt	480
715 gatgggtttttaattgggt tggtttttttttgggttccctata atg aat aatg	525
716 Met Ser Gln	
717 1	
719 act ttt tac cgc tgt aat aaa gga gaa atc atg agc aaa act atc gcg	583
720 Thr Phe Tyr Arg Cys Asn Lys Gly Glu Ile Met Ser Lys Thr Ile Ala	
721 5 10 15	
723 acg gaa aat gca ccg gca gct atc ggt cct tac gta cag ggc gtt gat	631
724 Thr Glu Asn Ala Pro Ala Ala Ile Gly Pro Tyr Val Gln Gly Val Asp	
725 20 25 30 35	
727 ctg ggc aat atg atc atc acc tcc ggt cag atc ccg gta aat ccg aaa	679
728 Leu Gly Asn Met Ile Ile Thr Ser Gly Gln Ile Pro Val Asn Pro Lys	
729 40 45 50	
731 acg ggc gaa gta ccg gca gac gtc gct gca cag gca cgt cag tcg ctg	727
732 Thr Gly Glu Val Pro Ala Asp Val Ala Ala Gln Ala Arg Gln Ser Leu	
733 55 60 65	
735 gat aac gta aaa gcg atc gtc gaa gcc gct ggc ctg aaa gtg ggc gac	775
736 Asp Asn Val Lys Ala Ile Val Glu Ala Ala Gly Leu Lys Val Gly Asp	
737 70 75 80	
739 atc gtt aaa act acc gtg ttt gta aaa gat ctg aac gac ttc gca acc	823
740 Ile Val Lys Thr Thr Val Phe Val Lys Asp Leu Asn Asp Phe Ala Thr	
741 85 90 95	
743 gta aac gcc act tac gaa gcc ttc ttc acc gaa cac aac gcc acc ttc	871
744 Val Asn Ala Thr Tyr Glu Ala Phe Phe Thr Glu His Asn Ala Thr Phe	
745 100 105 110 115	
747 ccg gca cgt tct tgc gtt gaa gtt gcc cgt ctg ccg aaa gac gtg aag	919
748 Pro Ala Arg Ser Cys Val Glu Val Ala Arg Leu Pro Lys Asp Val Lys	
749 120 125 130	
752 att gag atc gaa gcg atc gct gtt cgt cgc taa tcttgatgga aatccgggt	972
753 Ile Glu Ile Glu Ala Ile Ala Val Arg Arg	
754 135 140	
756 atcatgccc gattaagtct gatgacaaac gcaaaatcgc ctgatgcgt acgcttatca	1032

RAW SEQUENCE LISTING
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Input Set : A:\pto.da.txt
Output Set: N:\CRF4\02282006\J567749.raw

758	ggcctacgtg	attcctgcaa	tttattgaat	ttgttggccg	gataaggcat	ttacgcccga	1092
760	tccggcatga	acaaaactca	ctttgtctac	aatctgaatc	ggggctatcg	tgcccagtt	1152
762	attctttatt	gccagccgt	acgacggcta	tagaaccctt	tcaccaactg	ggttaatgtc	1212
764	atataccctg	ccagaatcgc	aaccagccac	gggaaatagc	ttaacggcag	cgcctgtaat	1272
766	tgcagataac	tggccagcgg	tgaaaacggc	aatgcgatcc	cgacaatcat	cacgatcacg	1332
768	gtcatgatca	ttaacggcca	cgatgcacag	ctctgaataa	acggcacacg	gcgggtgcgg	1392
770	atcatatgca	caatcagcgt	ttgcgacagt	aagcccacca	caaaccatcc	cgactggAAC	1452
772	agcgTTTgcg	tttccggcgt	gttggcatgg	aatacccacc	acatcaggca	aaacgtcaaa	1512
774	atATCGAAGA	tcgagctgat	cggtccgaag	aagatc			1548

E--> 777 <210> SEQ ID NO: 10<211> 141<212> PRT<213>. Escherichia coli

E--> 778 -

E--> 778 .

E--> 778 ::

W--> 778 <400> SEQUENCE: 10

779	Met Ser Gln Thr Phe Tyr Arg Cys Asn Lys Gly Glu Ile Met Ser Lys						
780	1	5	10	15			
782	Thr Ile Ala Thr Glu Asn Ala Pro Ala Ala Ile Gly Pro Tyr Val Gln						
783	20	25	30				
785	Gly Val Asp Leu Gly Asn Met Ile Ile Thr Ser Gly Gln Ile Pro Val						
786	35	40	45				
788	Asn Pro Lys Thr Gly Glu Val Pro Ala Asp Val Ala Ala Gln Ala Arg						
789	50	55	60				
791	Gln Ser Leu Asp Asn Val Lys Ala Ile Val Glu Ala Ala Gly Leu Lys						
792	65	70	75	80			
794	Val Gly Asp Ile Val Lys Thr Thr Val Phe Val Lys Asp Leu Asn Asp						
795	85	90	95				
797	Phe Ala Thr Val Asn Ala Thr Tyr Glu Ala Phe Phe Thr Glu His Asn						
798	100	105	110				
800	Ala Thr Phe Pro Ala Arg Ser Cys Val Glu Val Ala Arg Leu Pro Lys						
801	115	120	125				
803	Asp Val Lys Ile Glu Ile Glu Ala Ile Ala Val Arg Arg						
804	130	135	140				

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/567,749

DATE: 02/28/2006

TIME: 12:03:11

Input Set : A:\pto.da.txt

Output Set: N:\CRF4\02282006\J567749.raw

L:4 M:270 C: Current Application Number differs, Replaced Current Application No
 L:4 M:271 C: Current Filing Date differs, Replaced Current Filing Date
 L:0 M:282 E: Numeric Field Identifier Missing, <120> TITLE INVENTION
 L:0 M:201 W: Mandatory field data missing, <130> FILE REFERENCE
 L:4 M:283 W: Missing Blank Line separator, <160> field identifier
 L:5 M:281 W: Numeric Fields not Ordered, <220> not ordered!.
 L:5 M:283 W: Missing Blank Line separator, <220> field identifier
 L:5 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
 L:7 M:282 E: Numeric Field Identifier Missing, <210> is required.
 L:7 M:282 E: Numeric Field Identifier Missing, <211> is required.
 L:7 M:282 E: Numeric Field Identifier Missing, <212> is required.
 L:7 M:282 E: Numeric Field Identifier Missing, <213> is required.
 L:7 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:1
 L:92 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO: 2<211> 330<212>
 PRT<213> Escherichia coli<400> 2
 L:93 M:282 E: Numeric Field Identifier Missing, <211> is required.
 L:93 M:282 E: Numeric Field Identifier Missing, <212> is required.
 L:93 M:282 E: Numeric Field Identifier Missing, <213> is required.
 L:93 M:212 E: Mandatory Header Field missing, <400> is required.
 L:157 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO: 3<211> 993<212>
 DNA<213> Escherichia coli<220><221> Allele<222>
 L:160 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
 L:162 M:282 E: Numeric Field Identifier Missing, <211> is required.
 L:162 M:282 E: Numeric Field Identifier Missing, <212> is required.
 L:162 M:282 E: Numeric Field Identifier Missing, <213> is required.
 L:197 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO: 4<211> 75<212>
 DNA<213> Escherichia coli<220><221> tRNA<222>
 L:200 M:282 E: Numeric Field Identifier Missing, <211> is required.
 L:200 M:282 E: Numeric Field Identifier Missing, <212> is required.
 L:200 M:282 E: Numeric Field Identifier Missing, <213> is required.
 L:200 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:4
 L:207 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO: 5<211> 1545<212>
 DNA<213> Escherichia coli<220><221> CDS<222>
 L:210 M:282 E: Numeric Field Identifier Missing, <211> is required.
 L:210 M:282 E: Numeric Field Identifier Missing, <212> is required.
 L:210 M:282 E: Numeric Field Identifier Missing, <213> is required.
 L:210 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:5
 L:345 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO: 6<211> 514<212>
 PRT<213> Escherichia coli
 L:346 M:282 E: Numeric Field Identifier Missing, <211> is required.
 L:346 M:282 E: Numeric Field Identifier Missing, <212> is required.
 L:346 M:282 E: Numeric Field Identifier Missing, <213> is required.
 L:346 M:283 W: Missing Blank Line separator, <400> field identifier
 L:447 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO: 7<211> 1545<212>
 DNA<213> Escherichia coli
 L:449 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
 L:452 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
 L:455 M:282 E: Numeric Field Identifier Missing, <211> is required.
 L:455 M:282 E: Numeric Field Identifier Missing, <212> is required.
 L:455 M:282 E: Numeric Field Identifier Missing, <213> is required.
 L:590 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO: 8<211> 514<212>
 PRT<213> Escherichia coli
 L:591 M:282 E: Numeric Field Identifier Missing, <211> is required.

L:591 M:282 E: Numeric Field Identifier Missing, <212> is required.
L:591 M:282 E: Numeric Field Identifier Missing, <213> is required.

VERIFICATION SUMMARY
PATENT APPLICATION: US/10/567,749

DATE: 02/28/2006
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Input Set : A:\pto.da.txt
Output Set: N:\CRF4\02282006\J567749.raw

L:591 M:283 W: Missing Blank Line separator, <400> field identifier
L:692 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO: 9<211> 1548<212>
DNA<213> Escherichia coli
L:694 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:695 M:283 W: Missing Blank Line separator, <220> field identifier
L:695 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:698 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:698 M:282 E: Numeric Field Identifier Missing, <212> is required.
L:698 M:282 E: Numeric Field Identifier Missing, <213> is required.
L:777 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO: 10<211> 141<212>
PRT<213> Escherichia coli
L:778 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:778 M:282 E: Numeric Field Identifier Missing, <212> is required.
L:778 M:282 E: Numeric Field Identifier Missing, <213> is required.
L:778 M:283 W: Missing Blank Line separator, <400> field identifier
L:4 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (10) Counted (9) /

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